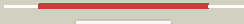

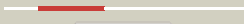














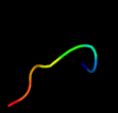




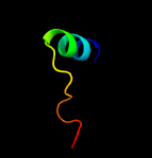
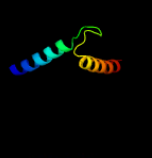
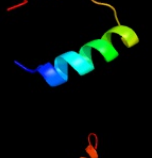
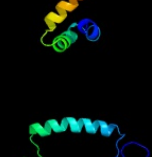

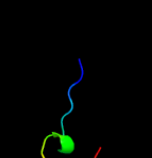
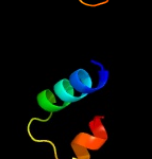

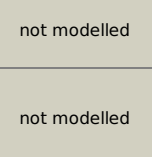


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0069c\_sdaA\_76234\_77619  
 Date Tue Jul 23 14:50:10 BST 2019  
 Unique Job ID 0154d1218c6018c1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4rqoB_</a>	 Alignment		100.0	50	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> l-serine dehydratase; <b>PDBTitle:</b> crystal structure of l-serine dehydratase from legionella pneumophila
2	<a href="#">d2iafa1</a>	 Alignment		100.0	42	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Serine metabolism enzymes domain <b>Family:</b> Serine dehydratase beta chain-like
3	<a href="#">c1ygyA_</a>	 Alignment		99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
4	<a href="#">d1ygya4</a>	 Alignment		99.4	20	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Serine metabolism enzymes domain <b>Family:</b> SerA intervening domain-like
5	<a href="#">d1szqa_</a>	 Alignment		97.6	20	<b>Fold:</b> 2-methylcitrate dehydratase PrpD <b>Superfamily:</b> 2-methylcitrate dehydratase PrpD <b>Family:</b> 2-methylcitrate dehydratase PrpD
6	<a href="#">c2hp0A_</a>	 Alignment		97.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ids-epimerase; <b>PDBTitle:</b> crystal structure of iminodisuccinate epimerase
7	<a href="#">c5muxB_</a>	 Alignment		96.5	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-methylcitrate dehydratase; <b>PDBTitle:</b> crystal structure of 2-methylcitrate dehydratase (mmge) from bacillus2 subtilis.
8	<a href="#">c4zhiA_</a>	 Alignment		48.9	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mg-chelatase subunit chlH; <b>PDBTitle:</b> crystal structure of the catalytic subunit of magnesium chelatase
9	<a href="#">c2m2rA_</a>	 Alignment		46.6	75	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> inhibitor cystine knot peptide mch-2; <b>PDBTitle:</b> solution structure of mch-2: a novel inhibitor cystine knot peptide2 from momordica charantia
10	<a href="#">c2w4eA_</a>	 Alignment		45.6	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mutt/nudix family protein; <b>PDBTitle:</b> structure of an n-terminally truncated nudix hydrolase2 dr2204 from deinococcus radiodurans
11	<a href="#">c3u4gA_</a>	 Alignment		36.9	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> namn:dmb phosphoribosyltransferase; <b>PDBTitle:</b> the structure of cobt from pyrococcus horikoshii

12	<a href="#">c6b2zd</a>	Alignment		35.5	24	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> atp synthase subunit c, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
13	<a href="#">c3j9eD</a>	Alignment		35.4	21	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> vp5; <b>PDBTitle:</b> atomic structure of a non-enveloped virus reveals ph sensors for a2 coordinated process of cell entry
14	<a href="#">c3s1sA</a>	Alignment		30.5	35	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> A: <b>PDB Molecule:</b> restriction endonuclease bpusi; <b>PDBTitle:</b> characterization and crystal structure of the type iig restriction2 endonuclease bpusi
15	<a href="#">d1ug2a</a>	Alignment		30.0	13	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
16	<a href="#">c5oynB</a>	Alignment		27.4	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dehydratase, ilvd/edd family; <b>PDBTitle:</b> crystal structure of d-xylonate dehydratase in holo-form
17	<a href="#">c5cagA</a>	Alignment		26.1	27	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative adhesin (bacova_02677) from2 bacteroides ovatus atcc 8483 at 3.00 a resolution (psi community3 target, nakayama)
18	<a href="#">d1no5a</a>	Alignment		23.1	28	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
19	<a href="#">d1rm6c1</a>	Alignment		22.8	12	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
20	<a href="#">d2i7pa1</a>	Alignment		22.5	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
21	<a href="#">d1ffva1</a>	Alignment	not modelled	20.4	12	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
22	<a href="#">c2zfdB</a>	Alignment	not modelled	20.1	25	<b>PDB header:</b> signaling protein/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein t20115_90; <b>PDBTitle:</b> the crystal structure of plant specific calcium binding protein atcb122 in complex with the regulatory domain of atc1pk14
23	<a href="#">c2i7pA</a>	Alignment	not modelled	20.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase 3; <b>PDBTitle:</b> crystal structure of human pank3 in complex with accoa
24	<a href="#">d2i7na2</a>	Alignment	not modelled	19.1	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Fumble-like
25	<a href="#">c1yy3A</a>	Alignment	not modelled	18.7	57	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosylmethionine:trna ribosyltransferase- <b>PDBTitle:</b> structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
26	<a href="#">d1fh9a</a>	Alignment	not modelled	18.1	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
27	<a href="#">c5xzoA</a>	Alignment	not modelled	18.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of gh10 xylanase xyl10c from bispora. sp mey-1
28	<a href="#">d1zxia1</a>	Alignment	not modelled	17.8	4	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like

29	<a href="#">d1v97a1</a>	Alignment	not modelled	17.5	4	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
30	<a href="#">d1ncfb3</a>	Alignment	not modelled	16.2	40	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
31	<a href="#">c5mrjA</a>	Alignment	not modelled	16.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-xylanase-like protein from2 acremonium chrysogenum
32	<a href="#">d1t3qa1</a>	Alignment	not modelled	15.9	12	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
33	<a href="#">c1knyA</a>	Alignment	not modelled	15.6	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> kanamycin nucleotidyltransferase; <b>PDBTitle:</b> kanamycin nucleotidyltransferase
34	<a href="#">c6mbdD</a>	Alignment	not modelled	15.4	28	<b>PDB header:</b> apoptosis <b>Chain:</b> D: <b>PDB Molecule:</b> dm1; <b>PDBTitle:</b> human mcl-1 in complex with the designed peptide dm1
35	<a href="#">c6mbdC</a>	Alignment	not modelled	15.4	28	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> dm1; <b>PDBTitle:</b> human mcl-1 in complex with the designed peptide dm1
36	<a href="#">c4i7hA</a>	Alignment	not modelled	15.2	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> peroxide stress sensing regulator; <b>PDBTitle:</b> structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
37	<a href="#">c6fheA</a>	Alignment	not modelled	15.0	8	<b>PDB header:</b> artificial enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> synthetic construct; <b>PDBTitle:</b> highly active enzymes by automated modular backbone assembly and2 sequence design
38	<a href="#">d1r85a</a>	Alignment	not modelled	14.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
39	<a href="#">d1uh6a</a>	Alignment	not modelled	14.5	23	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
40	<a href="#">c6hulB</a>	Alignment	not modelled	14.0	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan synthase beta chain 1; <b>PDBTitle:</b> sulfolobus solfataricus tryptophan synthase ab complex
41	<a href="#">c1m94A</a>	Alignment	not modelled	13.7	15	<b>PDB header:</b> structural genomics, signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein ynr032c-a; <b>PDBTitle:</b> solution structure of the yeast ubiquitin-like modifier2 protein hub1
42	<a href="#">d1m94a</a>	Alignment	not modelled	13.7	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
43	<a href="#">d1n62a1</a>	Alignment	not modelled	13.7	4	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
44	<a href="#">c3wvnB</a>	Alignment	not modelled	13.7	36	<b>PDB header:</b> metal binding protein/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> orff; <b>PDBTitle:</b> crystal structure of lysz from thermus thermophilus complex with lysw
45	<a href="#">d1v6ya</a>	Alignment	not modelled	13.2	5	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
46	<a href="#">c6ahtA</a>	Alignment	not modelled	13.0	9	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical plasmid protein; <b>PDBTitle:</b> plasmid partitioning protein tubr from bacillus cereus
47	<a href="#">d1jb0L</a>	Alignment	not modelled	13.0	30	<b>Fold:</b> Photosystem I reaction center subunit XI, PsaL <b>Superfamily:</b> Photosystem I reaction center subunit XI, PsaL <b>Family:</b> Photosystem I reaction center subunit XI, PsaL
48	<a href="#">d1v6wa2</a>	Alignment	not modelled	12.9	5	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
49	<a href="#">c4upcA</a>	Alignment	not modelled	12.7	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> nicastrin; <b>PDBTitle:</b> structure of a extracellular domain
50	<a href="#">c3vpbF</a>	Alignment	not modelled	12.7	40	<b>PDB header:</b> ligase <b>Chain:</b> F: <b>PDB Molecule:</b> alpha-aminoadipate carrier protein lysw; <b>PDBTitle:</b> argx from sulfolobus tokodaii complexed with2 lysw/glu/adp/mg/zn/sulfate
51	<a href="#">c3b9jl</a>	Alignment	not modelled	12.7	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> xanthine oxidase; <b>PDBTitle:</b> structure of xanthine oxidase with 2-hydroxy-6-methylpurine
52	<a href="#">c3ibqA</a>	Alignment	not modelled	12.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxal kinase; <b>PDBTitle:</b> crystal structure of pyridoxal kinase from lactobacillus plantarum in2 complex with atp
53	<a href="#">d1tuxa</a>	Alignment	not modelled	12.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
54	<a href="#">d1v0la</a>	Alignment	not modelled	12.4	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
55	<a href="#">d1ylqa1</a>	Alignment	not modelled	12.4	30	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Catalytic subunit of bi-partite nucleotidyltransferase
						<b>Fold:</b> TIM beta/alpha-barrel

56	<a href="#">d1bg4a_</a>	Alignment	not modelled	12.4	13	<b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
57	<a href="#">d1ta3b_</a>	Alignment	not modelled	12.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
58	<a href="#">c5k3jA_</a>	Alignment	not modelled	12.2	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a oxidase; <b>PDBTitle:</b> crystals structure of acyl-coa oxidase-2 in caenorhabditis elegans2 bound with fad, ascaroside-coa, and atp
59	<a href="#">c4xx6A_</a>	Alignment	not modelled	12.2	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of a glycosylated endo-beta-1,4-xylanase (glycoside2 hydrolase family 10/gh10) enzyme from gloeophyllum trabeum
60	<a href="#">d1exta3</a>	Alignment	not modelled	12.1	40	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
61	<a href="#">c3smpA_</a>	Alignment	not modelled	12.0	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pantothenate kinase 1; <b>PDBTitle:</b> monoclinic crystal structure of human pantothenate kinase 1 alpha
62	<a href="#">c6fhfA_</a>	Alignment	not modelled	12.0	13	<b>PDB header:</b> artificial enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> design; <b>PDBTitle:</b> highly active enzymes by automated modular backbone assembly and2 sequence design
63	<a href="#">c4f8xA_</a>	Alignment	not modelled	11.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> endo-1,4-beta-xylanase; <b>PDBTitle:</b> penicillium canescens endo-1,4-beta-xylanase xyle
64	<a href="#">c1rm6F_</a>	Alignment	not modelled	11.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa reductase gamma subunit; <b>PDBTitle:</b> structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
65	<a href="#">c5y6qA_</a>	Alignment	not modelled	11.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidase small subunit; <b>PDBTitle:</b> crystal structure of an aldehyde oxidase from methylobacillus sp.2 ky4400
66	<a href="#">c3dwwA_</a>	Alignment	not modelled	11.4	8	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cysteine synthase b; <b>PDBTitle:</b> crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
67	<a href="#">c2rkbE_</a>	Alignment	not modelled	11.3	10	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> serine dehydratase-like; <b>PDBTitle:</b> serine dehydratase like-1 from human cancer cells
68	<a href="#">c2rffA_</a>	Alignment	not modelled	11.3	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative nucleotidyltransferase; <b>PDBTitle:</b> crystal structure of a putative nucleotidyltransferase (np_343093.1)2 from sulfolobus solfataricus at 1.40 a resolution
69	<a href="#">c5ys9A_</a>	Alignment	not modelled	11.2	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coenzyme a oxidase 3; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase3 from yarrowia lipolytica
70	<a href="#">c3w26A_</a>	Alignment	not modelled	11.0	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycoside hydrolase family 10; <b>PDBTitle:</b> the high-resolution crystal structure of tsxyla, intracellular2 xylanase from /thermoanaerobacterium saccharolyticum jw/sl-ys485/:3 the complex of the e146a mutant with xylotriose
71	<a href="#">c5k3iH_</a>	Alignment	not modelled	10.9	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> acyl-coenzyme a oxidase; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase-1 in caenorhabditis elegans2 complexed with fad and atp
72	<a href="#">d1h72c1</a>	Alignment	not modelled	10.9	33	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> GHMP Kinase, N-terminal domain
73	<a href="#">c5nqgB_</a>	Alignment	not modelled	10.8	63	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> ron2; <b>PDBTitle:</b> crystal structure of plasmodium vivax ama1 in complex with a 39 aa2 pvron2 peptide
74	<a href="#">c4qysA_</a>	Alignment	not modelled	10.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase beta chain 2; <b>PDBTitle:</b> trpb2 enzymes
75	<a href="#">d1knya2</a>	Alignment	not modelled	10.8	16	<b>Fold:</b> Nucleotidyltransferase <b>Superfamily:</b> Nucleotidyltransferase <b>Family:</b> Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
76	<a href="#">c2fglA_</a>	Alignment	not modelled	10.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alkaline thermostable endoxylanase; <b>PDBTitle:</b> an alkali thermostable f/10 xylanase from alkalophilic bacillus sp.2 ng-27
77	<a href="#">c1n60D_</a>	Alignment	not modelled	10.4	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> carbon monoxide dehydrogenase small chain; <b>PDBTitle:</b> crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
78	<a href="#">c2k9iB_</a>	Alignment	not modelled	10.4	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein orf56; <b>PDBTitle:</b> nmr structure of plasmid copy control protein orf56 from sulfolobus2 islandicus
79	<a href="#">c4pmyB_</a>	Alignment	not modelled	10.4	3	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> xylanase; <b>PDBTitle:</b> crystal structure of gh10 endo-b-1,4-xylanase (xy nb) from xanthomonas2 axonopodis pv citri complexed with xylose
80	<a href="#">d1i1wa_</a>	Alignment	not modelled	10.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> beta-glycanases
						<b>PDB header:</b> oxidoreductase

81	<a href="#">c3eubj_</a>	Alignment	not modelled	10.4	4	<b>Chain:</b> J; <b>PDB Molecule:</b> xanthine dehydrogenase/oxidase; <b>PDBTitle:</b> crystal structure of desulfo-xanthine oxidase with xanthine
82	<a href="#">c6ju2A_</a>	Alignment	not modelled	10.3	35	<b>PDB header:</b> viral protein/rna <b>Chain:</b> A; <b>PDB Molecule:</b> polymerase 3; <b>PDBTitle:</b> structure of influenza d virus polymerase bound to crna promoter in2 class 1
83	<a href="#">d1p0ra_</a>	Alignment	not modelled	10.0	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
84	<a href="#">d1rypa_</a>	Alignment	not modelled	10.0	11	<b>Fold:</b> Ntn hydrolase-like <b>Superfamily:</b> N-terminal nucleophile aminohydrolases (Ntn hydrolases) <b>Family:</b> Proteasome subunits
85	<a href="#">c1ffuA_</a>	Alignment	not modelled	9.9	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> cuts, iron-sulfur protein of carbon monoxide <b>PDBTitle:</b> carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
86	<a href="#">c2lr8A_</a>	Alignment	not modelled	9.9	16	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> casp8-associated protein 2; <b>PDBTitle:</b> solution nmr structure of casp8-associated protein 2 from homo2 sapiens, northeast structural genomics consortium (nesg) target3 hr8150a
87	<a href="#">c5y9dA_</a>	Alignment	not modelled	9.8	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coenzyme a oxidase 1; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase1 from yarrowia lipolytica
88	<a href="#">c2ddhA_</a>	Alignment	not modelled	9.8	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> acyl-coa oxidase; <b>PDBTitle:</b> crystal structure of acyl-coa oxidase complexed with 3-oh-dodecanoate
89	<a href="#">c4hx3H_</a>	Alignment	not modelled	9.7	50	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> H; <b>PDB Molecule:</b> neutral proteinase inhibitor scnpi; <b>PDBTitle:</b> crystal structure of streptomyces caespitosus sermetstatin in complex2 with s. caespitosus snapalysin
90	<a href="#">c5m0kB_</a>	Alignment	not modelled	9.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> crystal structure of endo-1,4-beta-xylanase from cellulomonas2 flavigena
91	<a href="#">c5oeiA_</a>	Alignment	not modelled	9.5	16	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein family upf0065:tat pathway signal; <b>PDBTitle:</b> r. palustris rpa4515 with oxoadipate
92	<a href="#">c2mpoA_</a>	Alignment	not modelled	9.4	67	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> mic2-associated protein; <b>PDBTitle:</b> structural basis of toxoplasma gondii mic2-associated protein2 interaction with mic2
93	<a href="#">c1us2A_</a>	Alignment	not modelled	9.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> endo-beta-1,4-xylanase; <b>PDBTitle:</b> xylanase10c (mutant e385a) from cellvibrio japonicus in complex with2 xylopentaose
94	<a href="#">d1pbya1</a>	Alignment	not modelled	9.2	14	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
95	<a href="#">c2zsjB_</a>	Alignment	not modelled	9.2	25	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> threonine synthase; <b>PDBTitle:</b> crystal structure of threonine synthase from aquifex aeolicus vf5
96	<a href="#">c5tzba_</a>	Alignment	not modelled	9.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> d-aminopeptidase; <b>PDBTitle:</b> burkholderia sp. beta-aminopeptidase
97	<a href="#">c6q8nB_</a>	Alignment	not modelled	9.1	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> beta-xylanase; <b>PDBTitle:</b> gh10 endo-xylanase in complex with xylobiose epoxide inhibitor
98	<a href="#">c3hrdH_</a>	Alignment	not modelled	9.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H; <b>PDB Molecule:</b> nicotinate dehydrogenase small fes subunit; <b>PDBTitle:</b> crystal structure of nicotinate dehydrogenase
99	<a href="#">d2nrha1</a>	Alignment	not modelled	9.1	6	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> CoaX-like